

PCT09

RAW SEQUENCE LISTING

DATE: 10/30/2001

PATENT APPLICATION: US/09/889,616

TIME: 12:48:09

Input Set : N:\Crf3\RULE60\09889616.txt

Output Set: N:\CRF3\10302001\I889616.raw

ENTERED

1 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
 2 TANG, Y. Tom
 3 LAL, Preeti
 4 HILLMAN, Jennifer L.
 5 YUE, Henry
 6 AZIMZAI, Yalda
 7 LU, Aina M.D.
 8 BAUGHN, Mariah R.
 9 TRAN, Bao
 10 SHIH, Leo L.
 11 AU-YOUNG, Janice
 W--> 12 <120> TITLE OF INVENTION: NUCLEIC ACID-BINDING PROTEINS
 W--> 13 <130> FILE REFERENCE: PF-0662 PCT
 15 <140> CURRENT APPLICATION NUMBER: 09/889,616
 16 <141> CURRENT FILING DATE: 2001-07-16
 18 <150> PRIOR APPLICATION NUMBER: PCT/US00/02237
 19 <151> PRIOR FILING DATE: 2000-01-28
 21 <160> NUMBER OF SEQ ID NOS: 110
 22 <170> SOFTWARE: PERL Program
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 754
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 W--> 28 <220> FEATURE:
 W--> 29 <221> NAME/KEY: misc-feature
 30 <223> OTHER INFORMATION: Incyte ID No.: 025733CD1
 W--> 31 <400> SEQUENCE: 1
 32 Met Ala Ala Ala Gly Ser Arg Lys Arg Arg Leu Ala Glu Leu Thr
 33 1 5 10 15
 34 Val Asp Glu Phe Leu Ala Ser Gly Phe Asp Ser Glu Ser Glu Ser
 35 20 25 30
 36 Glu Ser Glu Asn Ser Pro Gln Ala Glu Thr Arg Glu Ala Arg Glu
 37 35 40 45
 38 Ala Ala Arg Ser Pro Asp Lys Pro Gly Gly Ser Pro Ser Ala Ser
 39 50 55 60
 40 Arg Arg Lys Gly Arg Ala Ser Glu His Lys Asp Gln Leu Ser Arg
 41 65 70 75
 42 Leu Lys Asp Arg Asp Pro Glu Phe Tyr Lys Phe Leu Gln Glu Asn
 43 80 85 90
 44 Asp Gln Ser Leu Leu Asn Phe Ser Asp Ser Asp Ser Ser Glu Glu
 45 95 100 105
 46 Glu Glu Gly Pro Phe His Ser Leu Pro Asp Val Leu Glu Glu Ala
 47 110 115 120
 48 Ser Glu Glu Glu Asp Gly Ala Glu Glu Gly Glu Asp Gly Asp Arg
 49 125 130 135
 50 Val Pro Arg Gly Leu Lys Gly Lys Lys Asn Ser Val Pro Val Thr
 51 140 145 150

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52	Val	Ala	Met	Val	Glu	Arg	Trp	Lys	Gln	Ala	Ala	Lys	Gln	Arg	Leu
53					155					160					165
54	Thr	Pro	Lys	Leu	Phe	His	Glu	Val	Val	Gln	Ala	Phe	Arg	Ala	Ala
55					170					175					180
56	Val	Ala	Thr	Thr	Arg	Gly	Asp	Gln	Glu	Ser	Ala	Glu	Ala	Asn	Lys
57					185					190					195
58	Phe	Gln	Val	Thr	Asp	Ser	Ala	Ala	Phe	Asn	Ala	Leu	Val	Thr	Phe
59					200					205					210
60	Cys	Ile	Arg	Asp	Leu	Ile	Gly	Cys	Leu	Gln	Lys	Leu	Leu	Phe	Gly
61					215					220					225
62	Lys	Val	Ala	Lys	Asp	Ser	Ser	Arg	Met	Leu	Gln	Pro	Ser	Ser	Ser
63					230					235					240
64	Pro	Leu	Trp	Gly	Lys	Leu	Arg	Val	Asp	Ile	Lys	Ala	Tyr	Leu	Gly
65					245					250					255
66	Ser	Ala	Ile	Gln	Leu	Val	Ser	Cys	Leu	Ser	Glu	Thr	Thr	Val	Leu
67					260					265					270
68	Ala	Ala	Val	Leu	Arg	His	Ile	Ser	Val	Leu	Val	Pro	Cys	Phe	Leu
69					275					280					285
70	Thr	Phe	Pro	Lys	Gln	Cys	Arg	Met	Leu	Leu	Lys	Arg	Met	Val	Val
71					290					295					300
72	Val	Trp	Ser	Thr	Gly	Glu	Glu	Ser	Leu	Arg	Val	Leu	Ala	Phe	Leu
73					305					310					315
74	Val	Leu	Ser	Arg	Val	Cys	Arg	His	Lys	Lys	Asp	Thr	Phe	Leu	Gly
75					320					325					330
76	Pro	Val	Leu	Lys	Gln	Met	Tyr	Ile	Thr	Tyr	Val	Arg	Asn	Cys	Lys
77					335					340					345
78	Phe	Thr	Ser	Pro	Gly	Ala	Leu	Pro	Phe	Ile	Ser	Phe	Met	Gln	Trp
79					350					355					360
80	Thr	Leu	Thr	Glu	Leu	Leu	Ala	Leu	Glu	Pro	Gly	Val	Ala	Tyr	Gln
81					365					370					375
82	His	Ala	Phe	Leu	Tyr	Ile	Arg	Gln	Leu	Ala	Ile	His	Leu	Arg	Asn
83					380					385					390
84	Ala	Met	Thr	Thr	Arg	Lys	Lys	Glu	Thr	Tyr	Gln	Ser	Val	Tyr	Asn
85					395					400					405
86	Trp	Gln	Tyr	Val	His	Cys	Leu	Phe	Leu	Trp	Cys	Arg	Val	Leu	Ser
87					410					415					420
88	Thr	Ala	Gly	Pro	Ser	Glu	Ala	Leu	Gln	Pro	Leu	Val	Tyr	Pro	Leu
89					425					430					435
90	Ala	Gln	Val	Ile	Ile	Gly	Cys	Ile	Lys	Leu	Ile	Pro	Thr	Ala	Arg
91					440					445					450
92	Phe	Tyr	Pro	Leu	Arg	Met	His	Cys	Ile	Arg	Ala	Leu	Thr	Leu	Leu
93					455					460					465
94	Ser	Gly	Ser	Ser	Gly	Ala	Phe	Ile	Pro	Val	Leu	Pro	Phe	Ile	Leu
95					470					475					480
96	Glu	Met	Phe	Gln	Gln	Val	Asp	Phe	Asn	Arg	Lys	Pro	Gly	Arg	Met
97					485					490					495
98	Ser	Ser	Lys	Pro	Ile	Asn	Phe	Ser	Val	Ile	Leu	Lys	Leu	Ser	Asn
99					500					505					510
100	Val	Asn	Leu	Gln	Glu	Lys	Ala	Tyr	Arg	Asp	Gly	Leu	Val	Glu	Gln

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101		515		520		525
102	Leu Tyr Asp Leu Thr	Leu Glu Tyr Leu His	Ser Gln Ala His	Cys		
103		530		535		540
104	Ile Gly Phe Pro Glu	Leu Val Leu Pro Val	Val Leu Gln Leu	Lys		
105		545		550		555
106	Ser Phe Leu Arg Glu	Cys Lys Val Ala Asn	Tyr Cys Arg Gln	Val		
107		560		565		570
108	Gln Gln Leu Leu Gly	Lys Val Gln Glu Asn	Ser Ala Tyr Ile	Cys		
109		575		580		585
110	Ser Arg Arg Gln Arg	Val Ser Phe Gly Val	Ser Glu Gln Gln	Ala		
111		590		595		600
112	Val Glu Ala Trp Glu	Lys Leu Thr Arg Glu	Glu Gly Thr Pro	Leu		
113		605		610		615
114	Thr Leu Tyr Tyr Ser	His Trp Arg Lys Leu	Arg Asp Arg Glu	Ile		
115		620		625		630
116	Gln Leu Glu Ile Ser	Gly Lys Glu Arg Leu	Glu Asp Leu Asn	Phe		
117		635		640		645
118	Pro Glu Ile Lys Arg	Arg Lys Met Ala Asp	Arg Lys Asp Glu	Asp		
119		650		655		660
120	Arg Lys Gln Phe Lys	Asp Leu Phe Asp Leu	Asn Ser Ser Glu	Glu		
121		665		670		675
122	Asp Asp Thr Glu Gly	Phe Ser Glu Arg Gly	Ile Leu Arg Pro	Leu		
123		680		685		690
124	Ser Thr Arg His Gly	Val Glu Asp Asp Glu	Glu Asp Glu Glu	Glu		
125		695		700		705
126	Gly Glu Glu Asp Ser	Ser Asn Ser Glu Gly	Glu Trp Ser Trp	Asp		
127		710		715		720
128	Gly Asp Pro Asp Ala	Glu Ala Gly Leu Ala	Pro Gly Glu Leu	Gln		
129		725		730		735
130	Gln Leu Ala Gln Gly	Pro Glu Asp Glu Leu	Glu Asp Leu Gln	Leu		
131		740		745		750

132 Ser Glu Asp Asp

134 <210> SEQ ID NO: 2

135 <211> LENGTH: 593

136 <212> TYPE: PRT

137 <213> ORGANISM: Homo sapiens

W--> 138 <220> FEATURE:

W--> 139 <221> NAME/KEY: misc-feature

140 <223> OTHER INFORMATION: Incyte ID No.: 079702CD1

W--> 141 <400> SEQUENCE: 2

142	Met Arg Asp Ser Thr	Gly Ala Gly Asn Ser	Leu Val His Lys	Arg
143	1	5	10	15
144	Ser Pro Leu Arg Arg	Asn Gln Lys Thr Pro	Thr Ser Leu Thr	Lys
145		20	25	30
146	Leu Ser Leu Gln Asp	Gly His Lys Ala Lys	Lys Pro Ala Cys	Lys
147		35	40	45
148	Phe Glu Glu Gly Gln	Asp Val Leu Ala Arg	Trp Ser Asp Gly	Leu
149		50	55	60
150	Phe Tyr Leu Gly Thr	Ile Lys Lys Ile Asn	Ile Leu Lys Gln	Ser

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151		65		70		75
152	Cys Phe Ile Ile Phe Glu Asp Ser Ser Lys Ser Trp Val Leu Trp					
153		80		85		90
154	Lys Asp Ile Gln Thr Gly Ala Thr Gly Ser Gly Glu Met Val Cys					
155		95		100		105
156	Thr Ile Cys Gln Glu Glu Tyr Ser Glu Ala Pro Asn Glu Met Val					
157		110		115		120
158	Ile Cys Asp Lys Cys Gly Gln Gly Tyr His Gln Leu Cys His Thr					
159		125		130		135
160	Pro His Ile Asp Ser Ser Val Ile Asp Ser Asp Glu Lys Trp Leu					
161		140		145		150
162	Cys Arg Gln Cys Val Phe Ala Thr Thr Thr Lys Arg Gly Gly Ala					
163		155		160		165
164	Leu Lys Lys Gly Pro Asn Ala Lys Ala Leu Gln Val Met Lys Gln					
165		170		175		180
166	Thr Leu Pro Tyr Ser Val Ala Asp Leu Glu Trp Asp Ala Gly His					
167		185		190		195
168	Lys Thr Asn Val Gln Gln Cys Tyr Cys Tyr Cys Gly Gly Pro Gly					
169		200		205		210
170	Asp Trp Tyr Leu Lys Met Leu Gln Cys Cys Lys Cys Lys Gln Trp					
171		215		220		225
172	Phe His Glu Ala Cys Val Gln Cys Leu Gln Lys Pro Met Leu Phe					
173		230		235		240
174	Gly Asp Arg Phe Tyr Thr Phe Ile Cys Ser Val Cys Ser Ser Gly					
175		245		250		255
176	Pro Glu Tyr Leu Lys Arg Leu Pro Leu Gln Trp Val Asp Ile Ala					
177		260		265		270
178	His Leu Cys Leu Tyr Asn Leu Ser Val Ile His Lys Lys Lys Tyr					
179		275		280		285
180	Phe Asp Ser Glu Leu Glu Leu Met Thr Tyr Ile Asn Glu Asn Trp					
181		290		295		300
182	Asp Arg Leu His Pro Gly Glu Leu Ala Asp Thr Pro Lys Ser Glu					
183		305		310		315
184	Arg Tyr Glu His Val Leu Glu Ala Leu Asn Asp Tyr Lys Thr Met					
185		320		325		330
186	Phe Met Ser Gly Lys Glu Ile Lys Lys Lys Lys His Leu Phe Gly					
187		335		340		345
188	Leu Arg Ile Arg Val Pro Pro Val Pro Pro Asn Val Ala Phe Lys					
189		350		355		360
190	Ala Glu Lys Glu Pro Glu Gly Thr Ser His Glu Phe Lys Ile Lys					
191		365		370		375
192	Gly Arg Lys Ala Ser Lys Pro Ile Ser Asp Ser Arg Glu Val Ser					
193		380		385		390
194	Asn Gly Ile Glu Lys Lys Lys Lys Lys Lys Ser Val Gly Arg Pro					
195		395		400		405
196	Pro Gly Pro Tyr Thr Arg Lys Met Ile Gln Lys Thr Ala Glu Pro					
197		410		415		420
198	Leu Leu Asp Lys Glu Ser Ile Ser Glu Asn Pro Thr Leu Asp Leu					
199		425		430		435

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200   Pro Cys Ser Ile Gly Arg Thr Glu Gly Thr Ala His Ser Ser Asn
201               440               445               450
202   Thr Ser Asp Val Asp Phe Thr Gly Ala Ser Ser Ala Lys Glu Thr
203               455               460               465
204   Thr Ser Ser Ser Ile Ser Arg His Tyr Gly Leu Ser Asp Ser Arg
205               470               475               480
206   Lys Arg Thr Arg Thr Gly Arg Ser Trp Pro Ala Ala Ile Pro His
207               485               490               495
208   Leu Arg Arg Arg Arg Gly Arg Leu Pro Arg Arg Ala Leu Gln Thr
209               500               505               510
210   Gln Asn Ser Glu Ile Val Lys Asp Asp Glu Gly Lys Glu Asp Tyr
211               515               520               525
212   Gln Phe Asp Glu Leu Asn Thr Glu Ile Leu Asn Asn Leu Ala Asp
213               530               535               540
214   Gln Glu Leu Gln Leu Asn His Leu Lys Asn Ser Ile Thr Ser Tyr
215               545               550               555
216   Phe Gly Ala Ala Gly Arg Ile Ala Cys Gly Glu Lys Tyr Arg Val
217               560               565               570
218   Leu Ala Arg Arg Val Thr Leu Asp Gly Lys Val Gln Tyr Leu Val
219               575               580               585
220   Glu Trp Glu Gly Ala Thr Ala Ser
221               590

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223 <210> SEQ ID NO: 3

224 <211> LENGTH: 534

225 <212> TYPE: PRT

226 <213> ORGANISM: Homo sapiens

W--> 227 <220> FEATURE:

W--> 228 <221> NAME/KEY: misc-feature

229 <223> OTHER INFORMATION: Incyte ID No.: 116208CD1

W--> 230 <400> SEQUENCE: 3

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231   Met Arg Ala Leu His Leu Leu Lys Ser Gly Cys Ser Pro Ala Val
232       1               5               10               15
233   Gln Ile Lys Ile Arg Glu Leu Tyr Arg Arg Arg Tyr Pro Arg Thr
234               20               25               30
235   Leu Glu Gly Leu Ser Asp Leu Ser Thr Ile Lys Ser Ser Val Phe
236               35               40               45
237   Ser Leu Asp Gly Gly Ser Ser Pro Val Glu Pro Asp Leu Ala Val
238               50               55               60
239   Ala Gly Ile His Ser Leu Pro Ser Thr Ser Val Thr Pro His Ser
240               65               70               75
241   Pro Ser Ser Pro Val Gly Ser Val Leu Leu Gln Asp Thr Lys Pro
242               80               85               90
243   Thr Phe Glu Met Gln Gln Pro Ser Pro Pro Ile Pro Pro Val His
244               95              100             105
245   Pro Asp Val Gln Leu Lys Asn Leu Pro Phe Tyr Asp Val Leu Asp
246               110             115             120
247   Val Leu Ile Lys Pro Thr Ser Leu Val Gln Ser Ser Ile Gln Arg
248               125             130             135
249   Phe Gln Glu Lys Phe Phe Ile Phe Ala Leu Thr Pro Gln Gln Val

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Input Set : N:\Crf3\RULE60\09889616.txt

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L:12 M:283 W: Missing Blank Line separator, <120> field identifier
L:13 M:283 W: Missing Blank Line separator, <130> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:138 M:283 W: Missing Blank Line separator, <220> field identifier
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:141 M:283 W: Missing Blank Line separator, <400> field identifier
L:227 M:283 W: Missing Blank Line separator, <220> field identifier
L:228 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:230 M:283 W: Missing Blank Line separator, <400> field identifier
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:311 M:283 W: Missing Blank Line separator, <400> field identifier
L:351 M:283 W: Missing Blank Line separator, <220> field identifier
L:352 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:354 M:283 W: Missing Blank Line separator, <400> field identifier
L:436 M:283 W: Missing Blank Line separator, <220> field identifier
L:437 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:503 M:283 W: Missing Blank Line separator, <220> field identifier
L:504 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:506 M:283 W: Missing Blank Line separator, <400> field identifier
L:619 M:283 W: Missing Blank Line separator, <220> field identifier
L:620 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:622 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:283 W: Missing Blank Line separator, <220> field identifier
L:648 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:650 M:283 W: Missing Blank Line separator, <400> field identifier
L:688 M:283 W: Missing Blank Line separator, <220> field identifier
L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
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L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
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L:825 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
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L:989 M:283 W: Missing Blank Line separator, <400> field identifier
L:1053 M:283 W: Missing Blank Line separator, <220> field identifier
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L:1106 M:283 W: Missing Blank Line separator, <220> field identifier

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L:1215 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
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L:1280 M:283 W: Missing Blank Line separator, <400> field identifier
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L:1500 M:283 W: Missing Blank Line separator, <220> field identifier
L:1501 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:1503 M:283 W: Missing Blank Line separator, <400> field identifier
L:1629 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1683 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
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L:1880 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:1931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1956 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:2009 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
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L:2578 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
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L:2693 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:2730 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09889616.txt

Output Set: N:\CRF3\10302001\I889616.raw

L:2763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:2810 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:2851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51
L:4971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:5004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104
L:5190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110